AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph beginning at page 3, line 19, as follows:

One aspect of the invention is broadly defined as a method of aligning a query protein sequence with ~~a template consisting of~~ a set of pre-selected protein structures in a database, <u>one by one,</u> comprising the steps of: selecting an energy function, the energy function being a sum of energy parameters and weighting factors; determining values for weighting factors in the energy function; establishing linear programming (LP) constraints for threading (or aligning) the query protein sequence with each structure in the set of pre-selected protein structures in a database; and performing a linear programming analysis based on a linear programming formulation including the energy function under the constraints, ~~to optimally align the query protein with the template~~<u>outputting the structure to which the query sequence aligns with the best score</u>.

Please amend the paragraph beginning at page 3, line 28, as follows:

Another aspect of the invention is defined as ~~A~~ <u>a</u> method of alignment comprising the steps of: formulating the protein threading problem as a large scale integer programming problem; relaxing this problem to a linear programming problem; and solving the integer program by a branch-and-bound method.

Please amend the paragraph beginning at page 4, line 1, as follows:

A further aspect of the invention is defined as a system for aligning proteins comprising: a computer operable to align a query protein sequence with ~~a template consisting of~~ a set of pre-selected protein structures in database, by performing the steps of: selecting an energy function; determining values for weighting factors in the energy function; establishing linear programming (LP) constraints for threading (or aligning) the query protein sequence with

each structure in the set of pre-selected protein structures in a database; and performing a linear programming analysis based on a linear programming formulation including the energy function under the constraints, ~~to optimally align the query protein with the template~~<u>outputting the structure to which the query sequence aligns with the best score</u>.

Please amend the paragraph beginning at page 7, line 15, as follows:

The invention can be generally represented per the flow chart of **Figure 2.** Briefly, this figure presents a method of aligning a query protein with a ~~template~~ <u>set of pre-selected protein structures in a database</u> which proceeds as follows:

First, an energy function is selected, and appropriate weighting factors determined, per step **60.** Energy functions and various methods for determining weighting factors are known in the art. It is preferable though, that the energy function described above, be used.

Please amend the paragraph beginning at page 7, line 22, as follows:

Next, linear programming constraints are established for threading (or aligning) the query protein sequence to each of <u>the</u> pre-selected protein structures in the database, per step **62.** A detailed discussion follows on the various constraints that may be used. Clearly though, the invention does not turn on any particular set of constraints being employed.

Please amend the paragraph beginning at page 7, line 27, as follows:

Finally, a linear programming analysis based on the LP formulation generated at step **62**, is performed at step **64.** This LP analysis considers the energy function under the constraints, in an attempt to optimally align the query protein with ~~the template~~<u>each structure in the pre-selected database</u>.